

ALIGNMENTS

RESULT 1

CXAR_MOUSE

```

ID  CXAR_MOUSE      STANDARD;      PRT;      365 AA.
AC  P977792; O09052;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  01-MAR-2002 (Rel. 41, Last annotation update)
DE  Cocksackievirus and adenovirus receptor homolog precursor (mCAR).
GN  CXADR OR CAR.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Liver;
RX  MEDLINE=97190109; PubMed=9036860;
RA  Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA  Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT  "Isolation of a common receptor for Cocksackie B viruses and
RT  adenoviruses 2 and 5.";
RL  Science 275:1320-1323(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C3H/MAI;
RX  MEDLINE=97250541; PubMed=9096397;
RA  Tomko R.P., Xu R., Philipson L.;
RT  "HCAR and mCAR: the human and mouse cellular receptors for subgroup C
RT  adenoviruses and group B coxsackieviruses.";
RL  Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Liver;
RA  Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;
RT  "The murine CAR homologue (mCAR) is a receptor for coxsackie B
RT  viruses and adenoviruses.";
RL  Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC  -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; Y10320; CAA71368.1; -.
DR  EMBL; U90715; AAC53148.1; -.
DR  EMBL; Y11929; CAA72679.1; -.
DR  MGD; MGI:1201679; Cxadr.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003598; Ig_c2.
DR  InterPro; IPR003600; Ig_like.
DR  Pfam; PF00047; ig; 2.
DR  SMART; SM00410; IG_like; 1.

```

DR SMART; SM00408; IGc2; 1.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
 FT HOMOLOG.
 FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 340 365 VAAPNLSRMGAVPVMIPAQSKDGSIV -> FKYAYKTDGIT
 FT VV (IN REF. 2 AND 3).
 SQ SEQUENCE 365 AA; 39947 MW; 5445B4B52A34B2A2 CRC64;

Query Match 17.6%; Score 353.5; DB 1; Length 365;
 Best Local Similarity 27.8%; Pred. No. 1.8e-16;
 Matches 113; Conservative 71; Mismatches 156; Indels 67; Gaps 15;

Qy 9 VTNLLRFLFL-GLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSSQPWE 67
 : || | : | | : : : | : | : | : | : | : | :
 Db 1 MARLLCFVLLCGIADFT---SGLSITTPEQRIEKAKGETAYLPCKFTLSPE--DQGPLD 54
 Qy 68 VPFVMWFFKQKEKE--DQVLSYINGVTTSKPGVSLVY-----SMPSRNL 109
 : | : | : | : | : | : | : | : | : | : | : | :
 Db 55 IE---WLISPSDNQIVDQVIILYSG-----DKIYDNYYPDLKGRVHFTSNDVKSGDA 103
 Qy 110 SLRLEGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLPAPPSCRLQGVPVHGAN 169
 | : : | | : | | | | : | : | | | | : | : | : | :
 Db 104 SINVTNLQLSDIGTYQCKVK-----KAPGVANKKFLTLVLKPSGTRCFVDGSEEIGND 157
 Qy 170 VTLSCQSPRSKPAVQYQWDRQLPSFQTFAPAL-DVIRGSLSLTNLSSSMAGVYVCKAHN 228
 | : | : : | : | : | : | : | : | : | : | : | : |
 Db 158 FKLKCEPKEGSLPLQFEW-QKLSDSQTMPTPWLAEMTSPVISVKNASSEYSGTYSCTVQN 216
 Qy 229 EVGTAQCNTLE-VSTGPGAAGVAVVGTLVGLGLLAGLVLLYHRR---GKALEEPAND 284
 | : | : | : | : | : | : | : | : | : | : | : | :
 Db 217 RVGSDQCMLRLDVPPSNRAGTIAGAVIGTLLALVLIGAILFCCHRKRREEKYEKEVHHD 276
 Qy 285 IKEDAIAPRTLWPWKSSDTISKNGTLSSVTSARALRPPHGPPrPGALTPTPSLSSQALPS 344
 | : | : | : | : | : | : | : | : | : | : | : | :
 Db 277 IRED-----VPPPKSRTSTARSYIGSNHSSL-----GSMSPSNMEGYSKTQY 318
 Qy 345 PRLPTTDGAH-PQPISPIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
 : : | : | : | : | : | : | : | : | : | : | : | :
 Db 319 NQVPSEDFERAPQSPTLAPAKVAAPNLSRMGAVPVMIPAQSKDGSIV 365

RESULT 2

CXAR_HUMAN

ID CXAR_HUMAN STANDARD; PRT; 365 AA.

AC P78310; O00694;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Cocksackievirus and adenovirus receptor precursor (Cocksackievirus B-adenovirus receptor) (hCAR) (CVB3 binding protein).

GN CXADR OR CAR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97190109; PubMed=9036860;

RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,

RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;

RT "Isolation of a common receptor for Cocksackie B viruses and

RT adenoviruses 2 and 5.";

RL Science 275:1320-1323(1997).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97250541; PubMed=9096397;

RA Tomko R.P., Xu R., Philipson L.;

RT "hCAR and mCAR: the human and mouse cellular receptors for subgroup C

RT adenoviruses and group B coxsackieviruses.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20008750; PubMed=10543405;

RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,

RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human

RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

RP SEQUENCE FROM N.A.

RA Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;

RT "Sequence and expression of CXADR, the human gene for the

RT coxsackievirus and adenovirus receptor.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND

CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; Y07593; CAA68868.1; -.

DR EMBL; U90716; AAC51234.1; -.

DR EMBL; AF169366; AAF05908.1; -.

DR EMBL; AF169360; AAF05908.1; JOINED.

```

DR EMBL; AF169361; AAF05908.1; JOINED.
DR EMBL; AF169362; AAF05908.1; JOINED.
DR EMBL; AF169363; AAF05908.1; JOINED.
DR EMBL; AF169364; AAF05908.1; JOINED.
DR EMBL; AF169365; AAF05908.1; JOINED.
DR EMBL; AF200465; AAF24344.1; -.
DR MIM; 602621; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00408; IGC2; 1.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258 POTENTIAL.
FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.
FT DISULFID 41 120 BY SIMILARITY.
FT DISULFID 162 212 BY SIMILARITY.
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;

```

Query Match 17.0%; Score 343; DB 1; Length 365;
Best Local Similarity 27.5%; Pred. No. 9e-16;
Matches 106; Conservative 67; Mismatches 147; Indels 66; Gaps 14;

Qy	31	LQLHLHPANRLQAVEGGEVVLPAWYTLHGEVSSSQPWEVFPVMWFFK--QKEKEDQVLSYI	88
Db	20	LSITTPPEEMIEKAKGETAYLPCKFTLSPE--DQGPLDIE--WLISPADNQKVDQVIILY	74
Qy	89	NGVTTSKPGVSLVY-----SMPSRNLSLRLEGLQEKDSGPYSCSVNVQD	132
Db	75	SG-----DKIYDDYYPDLKGRVHFTSNDLKS GDASINVNTNLQLSDIGTYQCKVK---	123
Qy	133	KQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQWDRQLP	192
Db	124	---KAPGVANKKIHVLVVKPSGARC YVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLS	180
Qy	193	SFQTFFPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTL E-VSTGPGA AVVA	251
Db	181	SQKMPTSWLAEMTSSVISVKNASSEYS GTYSTVRNRVGS DQCLRLNVVPPSNKAGLIA	240
Qy	252	GAVVGTLVGLGLLAGLVLLYHRRGKALE---EPANDIKEDAIAPRTLWPWKSSDTISK	307
Db	241	GAIIGTLLALALI-GLIIFCCRKKRREEKYEKVHHDIRE D-----VPPPKSRTSTARS	293
Qy	308	GTLSSVTSARALRPPH--GPPRPGALTPTPSLSSQALP-SPRLPTTDGAHPQPISPIPG	364
Db	294	YIGSNHSSLGSMSPSNMEGYSKT-QYNQVPSEDFERTPQSPTLP-----PAK	339
Qy	365	VSSSGLSRMGAVPVMVPAQSQAGSLV	390
Db	340	VAAPNLSRMGAIPVMIPAQSKDGSIV	365